

GenCore version 5.1.7
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OM nucleic - nucleic search, using SW model

Run on: April 4, 2006, 11:28:39 ; Search time 1101 Seconds
(without alignments)
2981.311 Million cell updates/sec

Title: US-10-082-018a-2

Perfect score: 1088
Sequence: 1 gcagtaactcttcctcgtaat.....caccaccaccactact 1088

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 6709644 seqs, 1508466879 residues

Total number of hits satisfying chosen parameters: 13419288

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Pending Patents: NA, New: *
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2: /SIDS5/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /SIDS5/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /SIDS5/ptodata/2/pna/US08_NEW_COMB.seq:*
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6: /SIDS5/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq:*
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9: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq2:*
10: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq3:*
11: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq4:*
12: /SIDS5/ptodata/2/pna/US60_NEW_COMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	589	54.1	1176	US-11-039-880-6	Sequence 6, Appl1
2	588	54.0	1140	US-11-039-880-4	Sequence 4, Appl1
3	132.2	12.2	3673778	US-10-312-841A-1	Sequence 1, Appl1
4	109.8	10.1	908	US-11-331-032-6574	Sequence 6574, Ap
5	109.4	10.1	2300	US-60-762-056-35494	Sequence 35494, A
6	106.8	9.8	810	US-11-331-032-6400	Sequence 6400, Ap
7	106.8	9.8	1317241	PCT-US06-08981-73	Sequence 73, Appl
8	102.4	9.4	980	US-11-331-032-6399	Sequence 6399, Ap
9	102.4	9.4	1835834	PCT-US06-08981-72	Sequence 72, Appl
10	101	9.3	2540030	PCT-US06-08981-69	Sequence 69, Appl
11	100.2	9.2	988	US-11-331-032-7174	Sequence 7174, Ap
12	100	9.2	1038	US-11-360-355-15948	Sequence 15948, A
13	99.6	9.2	17265	US-60-740-736-152	Sequence 152, Ap
14	98.6	9.1	1971884	PCT-US06-08981-70	Sequence 70, Appl
15	98.6	9.1	899	US-11-353-150-24647	Sequence 24647, A
16	98.6	9.1	1317241	PCT-US06-08981-73	Sequence 73, Appl
17	98	9.0	2300	US-60-762-056-21229	Sequence 21229, A
18	97.2	8.9	777	US-11-331-032-1045	Sequence 1045, Ap
19	96.8	8.9	1202	US-11-360-355-22884	Sequence 22884, A
20	96.6	8.9	607	US-11-331-032-1335	Sequence 1335, Ap
21	95.8	8.8	1099	US-11-331-032-6603	Sequence 6603, Ap

22	95.8	8.8	1836	US-11-360-355-31136	Sequence 31136, A
23	95.8	8.8	3673778	US-10-312-841A-2	Sequence 2, Appl1
24	95.6	8.8	2501	PCT-US04-20336-369	Sequence 369, Ap
25	95.6	8.8	2501	US-10-506-111-1172	Sequence 172, Ap
26	95.6	8.8	2501	US-11-317-798-369	Sequence 369, Ap
27	95.6	8.8	3673778	US-10-312-841A-2	Sequence 2, Appl1
28	95.4	8.8	2540030	PCT-US06-08981-69	Sequence 69, Appl
29	94.2	8.7	17265	US-60-740-736-280	Sequence 280, Ap
30	94	8.6	2501	PCT-US04-20336-485	Sequence 485, Ap
31	94	8.6	2501	US-10-506-111-300	Sequence 300, Ap
32	94	8.6	2501	US-11-317-798-485	Sequence 485, Ap
33	92.4	8.5	2300	US-60-762-056-26311	Sequence 26311, A
34	92.2	8.5	11222	US-10-506-111-246	Sequence 246, Ap
35	92.2	8.5	11222	US-10-506-111-374	Sequence 374, Ap
36	92.2	8.5	1835834	PCT-US06-08981-72	Sequence 72, Appl
37	92	8.5	1971884	PCT-US06-08981-70	Sequence 70, Appl
38	91.8	8.4	576	US-11-331-032-6538	Sequence 5638, Ap
39	91.8	8.4	1097	US-11-331-032-6594	Sequence 6594, Ap
40	90.4	8.3	711	US-11-331-032-12583	Sequence 12583, A
41	90.2	8.3	664	US-11-331-032-6337	Sequence 6337, Ap
42	89.8	8.3	775	US-11-331-032-6390	Sequence 6390, Ap
43	89.6	8.2	706	US-11-331-032-6390	Sequence 6390, Ap
44	89.4	8.2	2300	US-60-762-056-4574	Sequence 4574, Ap
45	89.4	8.2	20420	US-11-375-555-385	Sequence 385, Ap

ALIGNMENTS

RESULT 1
US-11-039-880-6
Sequence 6, Application US/11039880
GENERAL INFORMATION:
APPLICANT: Lyon, Jeffrey A.
APPLICANT: Angov, Evelina
TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite
FILE REFERENCE: 003/241/SAP
CURRENT FILING DATE: 2006-01-24
PRIOR APPLICATION NUMBER: US/10/057,531
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/264,535
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/347,564
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 6
LENGTH: 1176
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: E. coli expressed P. falciparum MSP-142 (3D7)
US-11-039-880-6
Query Match 54.1%; Score 589; DB 8; Length 1176;
Best Local Similarity 72.7%; Pred. No. 5.8e-104;
Matches 819; Conservative 0; Mismatches 245; Indels 63; Gaps 2;
QY 4 GNACTCTTCGTAATGATTAACATCTTTCTTAATGAAATGAAATGAGGTTTA 63
DB 52 GCATATCTGTCAATGATTAATATCTCTCGAGTTTGAATAATGATGATGATTA 111
QY 64 TATTTAAACCTTACAGGTTTATTAAGTTTAAAAAACAATTAGAAATACGTT 123
DB 112 TATTTAAACCTTACAGGTTTATTAAGTTTAAAAAACAATTAGAAATACGTT 171
QY 124 ATGACATTTAATGTTAATGTTAAGATTTAATTTAATTCAGATTATTAACGTTAAAT 183
DB 172 TTATCATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 231
QY 184 TTCAAAATGTTTATGAAATGATTTAATTTCCATATTAATTAAGATTTAATCAATCAATTAAT 243

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OM nucleic - nucleic search, using bw model

Run on: April 4, 2006, 11:41:11, Search time 1446 Seconds
(without alignments)
3004.414 Million cell updates/sec

Title: US-10-082-018a-2

Perfect score: 1088

Sequence: 1 gacgaaccacccttcgtaat.....caccaccaccaccactaact 1088

Scoring table:

IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA New:*

- 1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 4: /SIDS5/ptodata/2/pubpna/PCr_NEW_PUB.seq:*
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- 14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277.4	25.5	279	14 US-11-144-833-3	Sequence 3, Appli
2	277.4	25.5	342	14 US-11-144-833-6	Sequence 6, Appli
3	185	17.0	291	14 US-11-144-833-1	Sequence 1, Appli
4	185	17.0	330	14 US-11-144-833-9	Sequence 9, Appli
5	185	17.0	354	14 US-11-144-833-4	Sequence 4, Appli
6	185	17.0	387	14 US-11-144-833-7	Sequence 7, Appli
7	93	8.5	1230	6 US-09-925-065A-77681	Sequence 77681, A
8	93	8.5	1230	9 US-10-301-480-178920	Sequence 178920,
9	93	8.5	1230	10 US-10-301-480-792329	Sequence 792329,
10	93	8.5	1230	14 US-11-121-086-25	Sequence 25, Appli
11	92.8	8.5	49979	8 US-10-985-561-13443	Sequence 13443, A
12	92.4	8.5	979	10 US-10-301-480-595013	Sequence 595013,
13	92.4	8.5	979	10 US-10-301-480-595014	Sequence 595014,
14	92.4	8.5	979	10 US-10-301-480-595015	Sequence 595015,
15	92.4	8.5	979	10 US-10-301-480-1208422	Sequence 1208422,
16	92.4	8.5	979	10 US-10-301-480-1208423	Sequence 1208423,
17	92.4	8.5	979	10 US-10-301-480-1208424	Sequence 1208424,
18	92.4	8.5	980	10 US-10-301-480-595016	Sequence 595016,

19	92.4	8.5	980	10 US-10-301-480-1208425	Sequence 1208425,
20	91.8	8.4	1230	6 US-09-925-065A-77682	Sequence 77682, A
21	91.8	8.4	1230	9 US-10-301-480-178921	Sequence 178921,
22	91.8	8.4	1230	10 US-10-301-480-792330	Sequence 792330,
23	91.4	8.4	1230	6 US-09-925-065A-77683	Sequence 77683, A
24	91.4	8.4	1230	6 US-09-925-065A-77684	Sequence 77684, A
25	91.4	8.4	1230	6 US-10-301-480-178922	Sequence 178922,
26	91.4	8.4	1230	9 US-10-301-480-178923	Sequence 178923,
27	91.4	8.4	1230	10 US-10-301-480-792331	Sequence 792331,
28	91.4	8.4	1230	10 US-10-301-480-792332	Sequence 792332,
29	90.8	8.3	139054	14 US-11-121-086-96	Sequence 96, Appli
30	88	8.1	687411	9 US-10-330-773-26	Sequence 26, Appli
31	84	7.7	26772	8 US-10-995-561-13313	Sequence 13313, A
32	84	7.7	54946	8 US-10-995-561-13479	Sequence 13479, A
33	83.8	7.7	171486	14 US-11-121-086-105	Sequence 105, App
34	83.4	7.7	171486	14 US-11-121-086-105	Sequence 105, App
35	83.2	7.6	173602	14 US-11-121-086-45	Sequence 45, Appli
36	82.2	7.6	139054	14 US-11-121-086-96	Sequence 96, Appli
37	82	7.5	49979	8 US-10-995-561-13443	Sequence 13443, A
38	80	7.4	990	10 US-10-301-480-568794	Sequence 568794,
39	80	7.4	990	10 US-10-301-480-589139	Sequence 589139,
40	79.8	7.3	633	10 US-10-301-480-589139	Sequence 589139,
41	79.8	7.3	633	10 US-10-301-480-589140	Sequence 589140,
42	79.8	7.3	633	10 US-10-301-480-1202548	Sequence 1202548,
43	79.8	7.3	633	10 US-10-301-480-1202549	Sequence 1202549,
44	79.4	7.3	5501	8 US-10-240-708-38	Sequence 38, Appli
45	79.2	7.3	990	10 US-10-301-480-568791	Sequence 568791,

ALIGNMENTS

RESULT 1
US-11-144-833-3
Sequence 3, Application US/1144833
Publication No. US20060018932A1
GENERAL INFORMATION:
APPLICANT: LONGACRE-ANDRE, SHIRLEY
APPLICANT: ROTH, CHARLES
APPLICANT: NATO, FARIDABANO
APPLICANT: BARNWELL, JOHN
APPLICANT: MENNIS, KANINI
TITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT
TITLE OF INVENTION: OF PLASMODIUM MSP-1
FILE REFERENCE: 0660-0139-0XPC
CURRENT FILING DATE: 2005-06-06
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: US/09/125, 031
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: FCT/FR97/00290
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: FR96/01822
PRIOR FILING DATE: 1996-02-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 279
TYPE: DNA
ORGANISM: Plasmodium falciparum
US-11-144-833-3
Query Match 25.5%, Score 277.4, DB 14, Length 279;
Best Local Similarity 99.6%, Pred. No. 1, 1e-27;
Matches 278; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 787 AACATTTCACACCAATGCGTAAACCAATGCGCAAAATTCGATGTTTCAG 846
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DB 1 AACATTTCACACCAATGCGTAAACCAATGCGCAAAATTCGATGTTTCAG 60
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QY 847 CATTAGATGAAGAAGATGTAATGTTTAAATTAACCAACAGAGGTGATAA 906
|||||
DB 61 CATTAGATGAAGAAGATGTAATGTTTAAATTAACCAACAGAGGTGATAA 120
|||||

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OM nucleic - nucleic search, using BW model

Run on: April 4, 2006, 11:34:31 / Search time 1029 Seconds

(without alignments)
8743.521 Million cell updates/sec

Title: US-10-082-018a-2

Perfect score: 1088
Sequence: 1 gcagtaactcctccgtaact.....caccaccaccacctaact 1088

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
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6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1088	100.0	1088	9	US-10-949-975-2
3	1088	100.0	1088	10	US-11-140-676-2
4	1074.8	99.8	1175	5	US-10-062-809-7
5	1074.8	99.8	1175	8	US-10-935-793-7
6	1074.8	99.8	1175	5	US-10-925-385-7
7	1065	97.9	1131	5	US-10-087-464-58
8	1065	97.9	1137	5	US-10-087-464-54
9	1065	97.9	4920	9	US-10-954-924-1
10	1065	97.9	5917	5	US-10-087-464-9
11	1060.2	97.4	1065	8	US-10-677-641-7
12	1057.4	97.2	1119	6	US-10-404-667-1
13	1046.2	96.2	1116	6	US-10-404-667-3
14	623.6	57.3	4838	9	US-10-954-924-6
15	623.6	57.3	4894	9	US-10-954-924-4
16	623.6	57.3	4940	9	US-10-954-924-2
17	609.6	56.0	1142	5	US-10-082-018-8
18	609.6	56.0	1142	9	US-10-949-975-8
19	609.6	56.0	1142	10	US-11-140-676-8
20	601	55.2	1065	5	US-10-082-018-1
21	601	55.2	1065	9	US-10-949-975-1
22	601	55.2	1065	10	US-11-140-676-1
23	597	54.9	1219	5	US-10-062-809-1

24	597	54.9	1219	8	US-10-935-793-1	Sequence 1, Appli
25	597	54.9	1219	9	US-10-925-385-1	Sequence 1, Appli
26	589	54.1	1176	6	US-10-057-531A-6	Sequence 6, Appli
27	589	54.1	1176	6	US-10-057-532A-6	Sequence 6, Appli
28	588	54.0	1140	6	US-10-057-531A-4	Sequence 4, Appli
29	588	54.0	1140	6	US-10-057-532A-4	Sequence 4, Appli
30	573.8	52.7	1065	8	US-10-677-641-9	Sequence 9, Appli
31	569.4	52.3	1116	6	US-10-404-667-4	Sequence 4, Appli
32	306.6	28.2	1235	5	US-10-098-514-13	Sequence 13, Appli
33	306.6	28.2	1235	5	US-10-062-809-6	Sequence 6, Appli
34	306.6	28.2	1235	8	US-10-935-793-6	Sequence 6, Appli
35	306.6	28.2	1235	9	US-10-925-385-6	Sequence 6, Appli
36	302.4	27.8	1203	5	US-10-062-809-17	Sequence 17, Appli
37	302.4	27.8	1203	8	US-10-935-793-17	Sequence 17, Appli
38	301.6	27.7	1149	5	US-10-098-514-3	Sequence 3, Appli
39	301.4	27.7	1149	5	US-10-098-514-1	Sequence 1, Appli
40	277.4	25.5	279	3	US-09-134-333-3	Sequence 3, Appli
41	277.4	25.5	342	3	US-09-134-333-6	Sequence 3, Appli
42	277	25.5	342	5	US-10-087-464-59	Sequence 59, Appli
43	194.4	17.9	3147	8	US-10-257-047-44	Sequence 44, Appli
44	193.4	17.8	309	8	US-10-257-047-43	Sequence 43, Appli
45	193.4	17.8	3147	8	US-10-257-047-45	Sequence 45, Appli

ALIGNMENTS

RESULT 1
US-10-082-018-2
; Sequence 2, Application US/10082018
; Publication No. US20020144299A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, Li How
; TITLE OF INVENTION: NOVEL MODIFIED MSP-1 NUCLEIC ACID SEQUENCES AND METHODS FOR INCREASING MRNA LEVELS AND PROTEIN
; TITLE OF INVENTION: EXPRESSIONS IN CELL SYSTEMS
; FILE REFERENCE: 107.637.121A
; CURRENT APPLICATION NUMBER: US/10/082, 018
; PRIOR APPLICATION NUMBER: 2002-02-20
; PRIOR APPLICATION NUMBER: US/09/175, 684
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1088
; TYPE: DNA
; ORGANISM: preferably, a bacterium, virus, or parasite
US-10-082-018-2

Query Match 100.0%; Score 1088; DB 5; Length 1088;
Best local similarity 100.0%; Pred. No. 1.2e-147; Indels 0; Gaps 0;
Matches 1088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 241 TATGTTGCAAGATCATATTAATTTCTTAATTAAGAAAAAGATTAATTTCTTAAGC 300

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2006, 10:34:40 ; Search time 4195 Seconds
(without alignments)
12134.528 Million cell updates/sec

Title: US-10-082-018a-2

Sequence: 1 ggcagtaactccttcgtaact.....caccaccaccactact 1088

Scoring table: IDENTITY NTC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hnc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	384	35.3	606 5	BU496794 PESTOab5
2	375.2	34.5	570 5	BU497996 PESTOab9
3	339.8	31.2	537 3	BI815756 PESTOab3
4	310.6	28.5	550 5	BU498549 PESTOab9
5	243	22.3	432 5	BO631144 PESTOab3
6	230	21.1	419 5	BO451367 PESTOab9
7	205.2	18.9	501 3	BI814631 PESTOab4
8	204.2	18.8	422 5	BO451709 PESTOab0
9	203.4	18.7	365 8	BO452445 PESTOab9
10	199.2	18.3	455 5	BO451036 PESTOab0
11	198.2	18.2	476 5	BO498112 PESTOab9
12	198.2	18.2	402 3	BI670649 PESTOab0
13	171	15.7	402 3	BI670649 PESTOab0
14	159.2	14.6	303 3	BI815239 PESTOab1
15	141.2	13.0	408 3	BI814931 PESTOab0
16	141.2	13.0	418 5	BO451572 PESTOab0
17	141.2	13.0	422 5	BO451661 PESTOab0
18	130	11.9	1254 10	AG349719 Mus muscu
19	129	11.9	1392 10	CG757503 P052-4-CO
20	125.6	11.5	1612 10	AG320745 Mus muscu
21	125.4	11.5	1268 10	AG347098 Mus muscu
22	125.4	11.5	1378 10	AG350209 Mus muscu

23	122.8	11.3	1101 10	CNS00EVL	AL069706 Drosophila
24	121.6	11.2	1015 10	CI135318	CI135318 ISB1-106P
25	121	11.1	945 11	CNS04DOK	AI285149 Tetradon
26	120.8	11.1	1380 1	AJ928744	AJ928744
27	120.2	11.0	542 3	BM167382	BM167382 EST569905
28	120.2	11.0	964 10	CG957121	CG957121 TCB52.1.C
29	120.2	11.0	1272 1	AJ927522	AJ927522 AJ927522
30	120.2	11.0	1456 10	AG382339	AG382339 Mus muscu
31	119.4	11.0	1536 10	CI078538	CI078538 CH216-151
32	119.2	11.0	1381 10	CI082000	CI082000 CH216-165
33	119	10.9	1260 1	AJ928742	AJ928742 AJ928742
34	119	10.9	1608 10	CI118721	CI118721 ISB1-72J8
35	118.6	10.9	725 3	BM160032	BM160032 EST562555
36	118.2	10.9	1696 10	AG346840	AG346840 Mus muscu
37	118	10.8	1238 8	AJ925855	AJ925855 AJ925855
38	117.4	10.8	1248 8	DN808090	DN808090 73970127
39	117.4	10.8	1594 10	CI038406	CI038406 CH216-46A
40	117	10.8	1348 10	CG749499	CG749499 P043-4-A0
41	116.6	10.7	2157 10	CI081966	CI081966 CH216-165
42	116.2	10.7	1224 10	CI077121	CI077121 CH216-143
43	115.8	10.6	1299 8	DN709204	DN709204 CIJ81-H10
44	115.8	10.6	1626 6	CF238805	CF238805 AGENCOURT
45	115.6	10.6	1260 10	CI491610	CI491610 SAIL_559_

ALIGNMENTS

RESULT 1
BU496794 606 bp mRNA linear EST 11-SEP-2002
LOCUS
DEFINITION
PESTOab58h11.y1 Plasmodium falciparum 3D7 asexual CDNA Plasmidium falciparum 3D7 CDNA 5' similar to TR:09TVG8 Q9TVG8 MSAL PROTEIN ; , mRNA sequence.

ACCESSION
BU496794.1 GI:22792988

VERSION
EST.

SOURCE
Plasmidium falciparum 3D7

ORGANISM
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmidium.

REFERENCE
1 (bases 1 to 606)

AUTHORS
Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D.,

Warr,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B.,

Bowers,Y., Gibbons,M., Rletter,E., Bennett,J., Jentee,B., Ronko,I.,

Teagareishill,I.,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A.,

Magnire,L., Richey,J., Watkins,J., Kennedy,S., Levinso,D.,

Waterson,R., Wilson,R. and Sibley,D.

Washu Plasmidium EST Project

Contact: L. David Sibley

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

Library was constructed by Deobam Chakrabarti DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: L. David Sibley

(sibley@wustl.edu), Washington University

Seq primer: -400P from Gbco

High quality sequence step: 428.

Location/Qualifiers

1..606

/organism="Plasmidium falciparum 3D7"

/mol_type="mRNA"

/db_xref="taxon:36329"

/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"

/clone_lib="Plasmidium falciparum 3D7 asexual CDNA"

/note="Vector: pBluescript SK plus; Site 1: EcoRI; Site 2:

XhoI; Library was constructed by Deobam Chakrabarti.

total RNA samples were isolated from mixed stage

seponin(0.1%) lysed P. falciparum 3D7 infected

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2006, 10:01:54 ; Search time 746 Seconds
(without alignments)
9720.088 Million cell updates/sec

Title: US-10-082-018a-2
Perfect score: 1088
Sequence: 1 gcagtaacctcttcgtaact.....caccaccaccactact 1088

Scoring table: IDENTITY NTC
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21.*
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3: geneseqn2000s:*
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5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2002b:*
8: geneseqn2003a:*
9: geneseqn2003b:*
10: geneseqn2003c:*
11: geneseqn2003d:*
12: geneseqn2004a:*
13: geneseqn2004b:*
14: geneseqn2005a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1088	100.0	1088	10	ABX15263
2	1088	100.0	1088	11	ADM66680
3	1088	100.0	1088	14	ADY84057
4	1086.4	99.9	1088	2	AAx56009
5	1086.4	99.9	1088	2	AAx25587
6	1074.8	98.8	1175	14	ADY21419
7	1074.8	98.8	1175	14	ADY21419
8	1074.8	98.8	1175	14	ADY21419
9	1073.2	98.6	1175	10	ADY21419
10	1065	97.9	1131	6	ADY47012
11	1065	97.9	1137	6	ADY47012
12	1065	97.9	1897	2	AAx7958
13	1065	97.9	1950	2	AAx7958
14	1065	97.9	5282	8	ABQ84134
15	1065	97.9	5917	6	AAx46980
16	1063.4	97.7	1896	2	AAx7957
17	1057.4	97.2	1119	10	ADY21419
18	1057	97.2	4940	2	AAx35363
19	1046.2	96.2	1116	10	ADY21419

20	1005.2	92.4	5760	1	AAx50530
21	632.2	58.1	1077	5	AAx68976
22	623.6	57.3	4940	2	AAx21451
23	609.6	56.0	1140	2	AAx56021
24	609.6	56.0	1140	2	AAx25593
25	609.6	56.0	1142	10	ABX15269
26	609.6	56.0	1142	11	ADM6686
27	609.6	56.0	1142	14	ADY84063
28	601	55.2	1065	2	AAx5586
29	601	55.2	1065	2	AAx5586
30	601	55.2	1065	10	ABX15262
31	601	55.2	1065	11	ADM6679
32	601	55.2	1065	14	ADY84056
33	598.2	55.0	5181	2	AAx80911
34	597	54.9	1219	6	ABV72261
35	597	54.9	1219	10	ADY21413
36	597	54.9	1219	14	ADY21413
37	597	54.9	1219	14	ADY21413
38	597	54.9	1219	14	ADY21413
39	589	54.1	1128	5	AAx89840
40	589	54.1	1176	6	ABN84474
41	589	54.1	1176	10	ABZ5888
42	589	54.1	1176	11	ADM6523
43	588	54.0	1140	6	ABN84473
44	588	54.0	1140	10	ABZ58887
45	588	54.0	1140	11	ADM6521

ALIGNMENTS

RESULT 1	ABX15263	standard; DNA; 1088 BP.
ID	ABX15263	standard; DNA; 1088 BP.
XX	ABX15263	
XX	20-MAR-2003	(first entry)
DT	XX	
XX	XX	
DE	P. falciparum MSP-1 C-terminus DNA.	
XX	XX	
KW	Malaria; dr; DNA vaccine; C-terminus; MSP-1; merozoite surface protein 1;	
KM	mutant; His tag.	
XX	XX	
OS	Plasmodium falciparum.	
OS	Synthetic.	
XX	XX	
XX	Key	Location/Qualifiers
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FT	FT	/*tag= b
FT	FT	/partial
FT	FT	/product= "MSP1 42/His tag"
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XX	XX	
PN	US2002144299-A1.	
XX	XX	
PD	03-OCT-2002.	
XX	XX	
PF	20-FEB-2002; 2002US-00082018.	
XX	XX	
PR	20-OCT-1997; 97US-0062592P.	
PR	15-MAY-1998; 98US-0085649P.	
XX	XX	
XX	20-OCT-1998; 98US-00175684.	
PA	(GENZ) GENZYME TRANSGENICS CORP.	
XX	XX	
PI	Chen LH, Meade HM;	
XX	XX	
DR	WPI; 2003-165819/16.	
XX	XX	
PT	P-PSDB; ABX07566.	
PT	Novel modified malaria merozoite surface protein-1 nucleic acid, useful	
PT	for increasing mRNA levels and expression of the protein in cell culture	

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2006, 10:21:16 ; Search time 5463 Seconds
(without alignments)
11320.826 Million cell updates/sec

Title: US-10-082-018a-2

Perfect score: 1088
Sequence: 1 gcagtaactcctccgtaat.....caccaccaccactact 1088

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sta:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1088	100.0	1088	6	BD072830 Novel mod
2	1088	100.0	1088	6	BD077370 Novel mod
3	1088	100.0	1088	6	CS133015 Sequence
4	1088	100.0	1088	6	AR359785 Sequence
5	1074.8	98.8	1175	6	AR636155 Sequence
6	1065	97.9	1065	2	PFASURPRO
7	1065	97.9	1131	2	AF325919
8	1065	97.9	1203	2	PFASPI
9	1065	97.9	1636	2	PFAMSP806
10	1065	97.9	1636	2	PFAMSP808
11	1065	97.9	1636	2	PFAMSP837
12	1065	97.9	1636	2	PFAMSP837
13	1065	97.9	1842	6	AR307176 Sequence
14	1065	97.9	1896	6	AR307174 Sequence
15	1065	97.9	1896	6	AR307175 Sequence
16	1065	97.9	1950	6	AR307175 Sequence
17	1065	97.9	4920	6	A92450
18	1065	97.9	5282	2	PFPI90

19	1065	97.9	5917	2	PPANT195	X02919 Plasmodium
20	1065	97.9	7038	2	PFPI195A	X15063 Plasmodium
21	1063.4	97.7	1636	2	PFAMSP828	D13360 Plasmodium
22	1063.4	97.7	1636	2	PFAMSP844	D13363 Plasmodium
23	1063.4	97.7	1785	6	AR307163	AR307163 Sequence
24	1061.8	97.6	1636	2	PFAMSP822	D13359 Plasmodium
25	1061.8	97.6	1636	2	PFAMSP834	D13361 Plasmodium
26	1005.2	92.4	5760	6	A04562	A04562 P.falciparu
27	1005.2	92.4	5760	6	B00656	B00656 CDNA encodi
28	935.2	86.0	5220	2	AJ786604	AJ786604 Plasmodi
29	834.2	76.7	1104	11	AY343089	AY343089 Synthetic
30	623.6	57.3	4940	6	A92451	A92451 Sequence 2
31	623.6	57.3	4940	11	CYB131294	AJ131294 Cloning v
32	609.6	56.0	1142	6	BD072836	BD072836 Novel mod
33	609.6	56.0	1142	6	BD077376	BD077376 Novel mod
34	609.6	56.0	1142	6	CS133021	CS133021 Sequence
35	609.6	56.0	1142	6	AR359791	AR359791 Sequence
36	602.8	55.4	1726	2	PFAMSP815	D13346 Plasmodium
37	602.8	55.4	1726	2	PFAMSP8351	D13348 Plasmodium
38	602.8	55.4	1726	2	PFAMSP8352	D13349 Plasmodium
39	602.8	55.4	1726	2	PFAMSP838	D13350 Plasmodium
40	602.8	55.4	1726	2	PFAMSP842	D13352 Plasmodium
41	602.8	55.4	1956	2	PFME28A1D	Z35329 P.falciparu
42	602.8	55.4	5067	2	AB116599	AB116599 Plasmodi
43	602.8	55.4	5085	2	AF218248	AF218248 Plasmodi
44	602.8	55.4	5100	2	AB116596	AB116596 Plasmodi
45	602.8	55.4	5243	2	AF062348	AF062348 Plasmodi

ALIGNMENTS

RESULT 1	BD072830	1088 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD072830				
DEFINITION	Novel modified MSP-1 nucleic acid sequences and methods for				
ACCESSION	BD072830				
VERSION	BD072830.1	GI:22618433			
KEYWORDS	JP 2001520048-A/2.				
SOURCE	JP 2001520048-A/2.				
ORGANISM	unidentified				
REFERENCE	unclassified				
AUTHORS	1 (bases 1 to 1088)				
TITLE	Chang, L.H. and Meade, H.				
JOURNAL	Novel modified MSP-1 nucleic acid sequences and methods for				
COMMENT	Increasing mRNA levels and protein expressions in cell systems				
OS	Patent: JP 2001520048-A 2 30-OCT-2001;				
PN	GENZYME TRANSGENICS CORP MAYO FOUNDATION FOR MEDICAL EDUCATION AND				
PD	RESEARCH				
PF	OS preferable, a bacterium, virus, or parasite				
PR	JP 2001520048-A/2				
PC	30-OCT-2001				
PC	20-OCT-1998 JP 2000517094				
PC	20-OCT-1997 US 60/062592, 15-MAY-1998 US 60/085649 PI				
PC	LI HOU CHANG, HARRY MEADE				
PC	CI2N15/09, A01K67/027, A61K35/76, A61K39/012, A61K48/00, C07K14/445, PC				
PC	CI2N1/21.				
CC	CI2N5/10, CI2N15/00, CI2N5/00				
CC	Novel modified MSP-1 nucleic acid sequences and methods for				
CC	increasing				
CC	mRNA levels and protein expressions in cell systems FH Key				
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ORIGIN					
Query Match	100.0%; Score 1088; DB 6; Length 1088;				